

[illegible]

Figure 3

10 20 30 40 50 60 70 80 90 100 110 120
GAATTCATCGTGGCAAGGCAGCCTGAATGGATGATGAACCTGGGGTCTTCAATGGAGGGCCAGACTCCTGGGTCTAGGGGATGAGGAGGGGAGGATCGGGTAGCTGGGACCA

130 140 150 160 170 180 190 200 210 220 230 240
GGTGAAGGGGCTGGGGCCCACTTCTGAGTCTCAGAGAGAAGCATCTGGGCTCTCAAGCACCTGAGTGGGAGGAGGAGGGTCTGGCTCTCTGGAAAAACCACTCTTGGACCAT

250 260 270 280 290 300 310 320 330 340 350 360
CTATGCAGATCAGCGAACAAGAAGAAATTTCTGGGCCCATCTGAATTTCTAAGTTTGGGGGAGGGGCTGATCTGACACTGAGGTTCCCTGATCCTCAGCAAGCGGCAATTGTCTGA

370 380 390 400 410 420 430 440 450 460 470 480
TGAAAGAAGCGACCGCATCTGAGACACAAGTATCCTGGCTTGGAAAGCTCTACCTGGCGTGGGCGCAACCTCAACCTCATCTGTCCCTGCTCAGATGCTCAGACCTGGACATCCGAGC

490 500 510 520 530 540 550 560 570 580 590 600
CTCTCTCTCTGATGCAATCTGTGTTTCTTCCACGAGAAGCCATCCAGGCCAGGCAGGTCTCTCTGAAATAACCTGGGGGAGGGGTGGCTGAAAGTCCCTGACTGGAGTTGG

610 620 630 640 650 660 670 680 690 700 710 720
CAGCGAAGCGAGGCCCTGGAGTGGGACCAGGAGGAGAAGCAGGTTGGCTAATTTCTGGAGCCCCAAGGGTGCAAGGGTAGGCTTCTGTGTCTGAGGAGGAGGGCTGGGGCTCTGG

730 740 750 760 770 780 790 800 810 820 830 840
ACTCTCGGTCTGAGGAGGAGGGGTGGGGGCCCTGGACTCTGGGTCTGAGGAGGAGGGTCTGGGCTGTACTCTCTGATCTGAGGAGGAGGGCTGGGAACTTGGGCTCTGGGT

850 860 870 880 890 900 910 920 930 940 950 960
CTGAGGGAGGAGGGAGCTTTGGTCTGGACTCTGGGTCTGAGGAGTAGGGGCTAGGGATCTGGACTCTGGGTCTGAGGAAGGAGGGCTGGGTCTGGACTCTGGGTCTGAGGAAG

970 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080
GAGGGCAGGGGGCTTGGACTCTGGGTCTGAGGAAGGAGGGGCCGGGAGCCTGGACTCTTAAGTCTGAGGGAGGAGGGTCTGGGGGCTGGACTCTGGGTCTGAGCAGAAGGCTCTGG

1090 1100 1110 1120 1130 1140 1150 1160 1170 1180 1190 1200
GTGCTGGGAGTCCCGAGCCTGGGAGATGATGGTTAAACTTCTGGGAATCAAGTCAAACTCCTGAGTCTTTGACATTGATGTATCTTGAATGGGAGGGTCACTCTGTGGGGAAGGATTAC

1210 1220 1230 1240 1250 1260 1270 1280 1290 1300 1310 1320
CCAGGTGCCCGAGGCAAGAGCTGAAGGCCAACAATGTTTCAGTATAATAAGAAAAATAGTTAGAATAAGAAATAGTTATCATACAAATAGATATAGAGATGATCATGGACAGTATCAATC

1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430 1440
ATTAGTGTAAACATTATTAATCATAGCTATTACTTTTATCTTTGTTGTATAACTAATATAACCAGGAAACAACCGGTGGGTATAGGTCAGTACTGAAGGACATTGTGAGAAAGTGA

1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560
CCTAGAAGGCAAGAGTGAGCTTCTGTACACCCGCATAAGGGCTCTTGAAGGCTCTTGGTCAAGCGGAAGCCAGTGTCTGGGAAGGACCCGTACTCAGCAGACCAAGAAAGG

1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680
GAATCTCCCTTTCTTGGAGGAGTCAGGGAACACTCTGCTCCACCAGCTTCTGTGGAGGCTGGGTATTATCTAGGCCTGGCCGAGTCATCCTGCTGCTGTGCTTCAATGGTCAGGC

1690 1700 1710 1720 1730 1740 1750 1760 1770 1780 1790 1800
TCTCTGTCTCTGCAATTTCTCCCGTACTCCTGGTCTCTCTTGAAGTCTGATAGATAGCGGTAGAAGAAATAGTGAAGCCCTTTTCTTTTCTTTTGGAGGGAGTCTCGCTC

Figure 3 (cont'd)

Sequence III (cont.)

1810	1820	1830	1840	1850	1860	1870	1880	1890	1900	1910	1920
TGTCCCCCAGGCTGGAGTGCAGTGGCGTGATCTCGGCTCACTGCAATCTCCGCTCTCTGGGTTACACACATTCTCTCGCTCACCTCCCAAATAGCTAGGACTACAGGCGGCTCCACC											
1930	1940	1950	1960	1970	1980	1990	2000	2010	2020	2030	2040
ACGGCGCCGGATAATTTTTTGTATTTTATGATAGACAGGGTTTACCCTGTATGCGCAGGATGGCTCCACCTCTCGCTTGTATGATCCGCGGCTCAGCCTCCCAAAGTGTGGGATT											
2050	2060	2070	2080	2090	2100	2110	2120	2130	2140	2150	2160
ACAGCGGTGAGCCACGCGCGCGCGCGAAATAGTGAAGTCTTAAAGTCTTTGATCTTTCTATAAGTCAGAGAGAAACGCTGACATATGCTGCTTCTCTTCTGCTTCGGCTGCC											
2170	2180	2190	2200	2210	2220	2230	2240	2250	2260	2270	2280
TAAAAGGAAGGGCCCTGTCCCATGATCAGTGACTTGCTTGACCTTATCAGTCATTTGGAGGACTCACCTCTTATCTCTGCCCCCTTGTCTGTATACAATAAATATCAGCGG											
2290	2300	2310	2320	2330	2340	2350	2360	2370	2380	2390	2400
CCCAAGCAATTCGGGGCACTACCGGCTCTCTGGCTCTGATGGTAGTGGTCCCCGGGCGCAGCTGTTTCTCTTTATCTCTTTGTCTTTGTCTTTATTTCTTACAATCTCTCTCTCT											
2410	2420	2430	2440	2450	2460	2470	2480	2490	2500	2510	2520
CACAGGGGAAGAACACCCACCGCGCAAGCGCGGTAGGGCTGGACCTACGTTAGCTGCGCTGCTCGGGTTTGGGATGCTGGAGTGGGCTTGGACGAGAGAAATGCTTTAATTAGG											
2530	2540	2550	2560	2570	2580	2590	2600	2610	2620	2630	2640
TGACAGGGCGGCGAGAGGCTTTGTCTTGTGCGCGCGAGCCACGGCGCGCGCTGACGGCGTGGAAACAGACCTGTTCCACTCCGCTCTCCAGCCTTGGAAATGTTGCTTCTGTCGAGT											
2650	2660	2670	2680	2690	2700	2710	2720	2730	2740	2750	2760
GCAGGTCTGGAAGTAGCAGTTTGGCACGGGACCTAGAATTTCCCAAAAGGAGTGACTAGGGCTGGGATTTGGAAATTTAGTGTGGACGGTGAAGCGGGGGGTGTGGGAGATCGGAG											
2770	2780	2790	2800	2810	2820	2830	2840	2850	2860	2870	2880
ACCTGTGTGGCGCGGAGCACTGCAGGCTTGAGGCGCTTCCGCGCTCCGGCGGCGAGCTTGCAAAACAGTTCTCCATCCCCAGGAGGACGGCGGAGAGGGCGGACGATCGCTCCACT											
2890	2900	2910	2920	2930	2940	2950	2960	2970	2980	2990	3000
CGCGCGGACAGGTGCGGGGGCGCTGCCACGCGCTGGGGCGTGGCCAGGCTCGAAGCACCCAGGTGTGCGGGGCGGACTCTAAGGCCGTGGCACCGGAAGAGAGGGCGGCGATTGGA											
3010	3020	3030	3040	3050	3060	3070	3080	3090	3100	3110	3120
CCTCCCGCTCCAGCATTGCAACTGGGGCGCTCGTCTCTGTGTCACGCAATGATGCTGGGCTGCTCAGAAGCCAGGTAGCTGCTTGGTGAAGCCTTCGCGGACGTCATACGCGG											
3130	3140	3150	3160	3170	3180	3190	3200	3210	3220	3230	3240
CGCGAGGGGACGGCGGCTCCCTGCATCCCGATCTGGGAGCGGTGGGCGCAGGGGCAATCGCTTAGCCCTTGGCTGGGCTCGGCGCAAGTGACGGCGGGGCTCCACCTTC											
3250	3260	3270	3280	3290	3300	3310	3320	3330	3340	3350	3360
CAGCCATCCGCGCGGCGCGGAGGGCGGACGCTGCGAGACTCCGCGCGCGGCCCTCTCTTCTCTCTCCCCAAGCCCTGCTGCCAGTCCGGACAGGCTGCGGAGGGGAGGGCTGC											
3370	3380	3390	3400	3410	3420	3430	3440	3450	3460	3470	3480
CGGGCGGATAGCGGACGCTGGCTTCAGGGCGGGCGGATGTGGCTGCTTTGGGAGGTTGGCTCGGCGCACGAAAGGAGGATGTGGATCTGCCACCTGCAAGCAGTCTCGGCG											
3490	3500	3510	3520	3530	3540	3550	3560	3570	3580	3590	3600
TAAGTGGGACTGCCCACTCAGTTGTTCTGGGACCCAGGAACAATCTTCAGAACCGAGGAGTGCACCCCCAACCTTCTCTCAGGCTTCTTCAAGGCCCTAGGAATCTCCGCGACC											

Figure 3 (cont'd)

3610 3620 3630 3640 3650 3660 3670 3680 3690 3700 3710 3720
 TCCCCAGCCATTACTCTCCAGGAACCAAGATGCTCTCCGCTCTGACCTCCAGCTCTCTTGTTTTACTTGAACATACTGGTTCCCATCACCACTCTGTGGTGGATTTTGGCGCTC

3730 3740 3750 3760 3770 3780 3790 3800 3810 3820 3830 3840
 ACAGACAGGTACTCTGAGAAACAGGCTGGTGGAAAGTCCAGTATCAGCGGAACCTACAGGAGGGGAGACTCGAGATTCTTCAGGAAAGGTGTAGGAACCTGAGCCACTTTCTTTTTT

3850 3860 3870 3880 3890 3900 3910 3920 3930 3940 3950 3960
 TTTTTTTTTTTTTTTTAAAGCAGGGTCCCTCTCTGTCCGCAAGCTGGAGTGCAGTCAGCGGTGCTATCGCGGCTCATTTGTGAGCTCCGGGGATCCCTCCGCCCTTAGCATCCGGGTAG

3970 3980 3990 4000 4010 4020 4030 4040 4050 4060 4070 4080
 CTGAGACCAGACATGTGCCACCATTGCCAAGCTAAATTTTATTTATTTTATTTTGGAGACGGAGTTTCACTCTGTGTGCCAGGCTGGAGTGAATGGCATGATCTCAGCTCACCGCAAC

4090 4100 4110 4120 4130 4140 4150 4160 4170 4180 4190 4200
 TCCCCCCCCCGGGTTCAGGCGATTCTCTGCTCAGCTCCCGAGTGGCTGGGATTACAGGCATGGCGCACCATGCCCGCTAAATTTGTATTTTAAAGTAGACAGGGTTCTCCAGC

4210 4220 4230 4240 4250 4260 4270 4280 4290 4300 4310 4320
 TTGGTCAGGCTGGTCTGAACTCCCAACTCAGGTGATCACCACCTTGGCTCCAAAGTGTGGGATACAGGTGTGAGCCACCGCGCTGCCCTGCCAAGCTAAATTTAAAAAT

4330 4340 4350 4360 4370 4380 4390 4400 4410 4420 4430 4440
 TTTTGTAAAGTGCTCTGTGCCAGGCTGATCTGAACTGGGGGTGAAGGATCTCCCATCTCAGCTCCCAATATGCTGGGATACAGGTGTGAGCCACAGTGGCCAGCCAAAC

4450 4460 4470 4480 4490 4500 4510 4520 4530 4540 4550 4560
 CATGGCTATCTTGAACCACTTGTCTTCAGTCCCCATGCCCAAAATTCGAAGGCTCTCATCCCTGAAACCTAGGACTCAGGCTCTCCCTACCTCAGCCCCAGGAGTCTAAACCTTTA

4570 4580 4590 4600 4610 4620 4630 4640 4650 4660 4670 4680
 ACTTCTCTTTCCTGGGACTAAGGAGTGTGCACCCAGCGCGCTCCCTACCCACATCTCCTCAGCTCCCTCTCAGCTCAGTGCAATTTGCTAACTGCCCTTCTCCCTCTG

4690 4700 4710 4720 4730 4740 4750 4760 4770 4780 4790 4800
 CAGCCATGTGGCTCCGAGGCCATGTCAGCTCTGGCTGGCTCTCTGCTAGTCTGTGCTCTCTCTGTAATCTCTTCTCTCCATATCCATCAAGCAGCTTTCCACATGGCCTAGGCCTGT
 MetTPluEArgSerHisArgInleuCysleuAlaPheLeuLeuValCysValLeuSerValIlePhePheLeuHisIleHisGlnAspSerPheProHisGlyLeuGlyLeuS

4810 4820 4830 4840 4850 4860 4870 4880 4890 4900 4910 4920
 CGATCCTGTGCTCCAGACCGCGCGCTGGTGACACCCAGTGGCATCTTCTGCCCTCGGGTACTGCGATGGGCGCCAAAGCGCTCCTCTCTCTGCCACGACCTCGTTCCCTCTCGG
 erIleLeuCysProAspArgArgLeuValThrProProValAlaIlePheCysLeuProGlyThrAlaMetGlyProAspAlaSerSerSerCysProGlnHisProAlaSerLeuSerG

4930 4940 4950 4960 4970 4980 4990 5000 5010 5020 5030 5040
 GCACCTGGAGCTGTCTACCCCAATGGCGGTTGGTAATCAGATGGGACAGTATGCCAGCTGCTGGCTCTGGCGGCTCAACGGCCGCCGGGCTTTATCTGCTGCCTGCCATGCATGCCG
 lyThrThrProValThrProAsnGlyArgPheGlyAsnGlnMetGlyGlnIleThrLeuLeuAlaLeuAlaGlnLeuAsnGlyArgArgAlaPheIleLeuProAlaMetHisAlaA

5050 5060 5070 5080 5090 5100 5110 5120 5130 5140 5150 5160
 CCTTGGCCCGGTATTCCGATCACCTGCCCTGCTGGCCCCAGAGTGAACGCCGACGCCGTGGCGGAGTGCAGCTTCACGACTGGATGTGGAGGAGTACGGGAGCTTGAGAG
 laLeuAlaProValPheArgIleThrLeuProValLeuAlaProGluValAspSerArgThrProTrpArgGluLeuGlnLeuHisAspTrpMetSerGluGluIleValAlaAspLeuArgA

5170 5180 5190 5200 5210 5220 5230 5240 5250 5260 5270 5280
 ATCCTTCTTGAAGCTCTTGGCTTCCCTGCTCTTGGACTTTCTCCACATCTCCGGGAACAGATCCGACAGAGATTCACTCCGACGACCACTTCGGGAAGAGGGGTGGTGGTGGC
 spProPheLeuLysLeuSerGlyPheProCysSerThrThrPhePheHisIleuArgGluGlnIleArgArgGluPheThrLeuHisAspHisLeuArgGluGluAlaGlnSerValI

5290 5300 5310 5320 5330 5340 5350 5360 5370 5380 5390 5400
 TGGGTGAGCTCCGCTGGCGGCAAGGGGACCGCCCGGACCTTTGTGGCGCTCAGCTGGCGGCTGGGAGCTATCTCAGGATTATGCTCAGCGCTGGAAGGGGTGGTGGTGGCGGACA
 euGlyGlnLeuArgLeuGlyArgThrGlyAspArgProArgThrPheValGlyValHisValArgArgGlyAspTyrLeuGlnValMetProGlnArgTrpLysGlyValValGlyAspS

Figure 3 (cont'd)

[illegible]

8170
TGGGEECACTGCAA

WILL
IN

[illegible]

2.

910	920	930	940	950	960
CCTTG ACAC AAGG	CCTTG GGGG	GGCCA CATCT	TCATC TTTCG	TTTAT GAGTC	CTGTG
970	980	990	1000	1010	1020
CGTCT TGTA CAAG	AATAC TACTA	TGAGC CGGCA	AGTCA GACTT	ATTTC GTAGG	GGACC
1030	1040	1050	1060	1070	1080
AAAGG AAAGA ACATG	TTTTG ATTGC	TAAGA AAACA	TTTTG TTCTC	TATCC TTTAC	TGGGC
1090	1100	1110	1120	1130	1140
TGGCA GGCAG	AGGAA ATGTT	CTTAT GAGCA	CTCAC ATTGA	AAACT TAAGT	CTCTC ACCAA
1150	1160	1170	1180	1190	1200
ATGCA GAGAC	TTTCA AGGCT	ATGCC GGTGC	GGGCT GGCTC	GAGAA TTGCA	GGCTC TCGGC
1210	1220	1230	1240	1250	1260
GGGCC ACAGG	ATGCT GGCCA	CGGAT GCGCT	GGCCG GGCCT	CTGCT CGCAC	GTTCG CCGCG
1270	1280	1290	1300	1310	1320
CGTCT GGACT	GGCTC CTGCC	CTCAA TCGCT	CGCTC GGGCG	GGGCT CGCTG	GGGGG TGGCT
1330	1340	1350	1360	1370	1380
AGGCC CACAG	CGAGG AAGCC	GAGCG TATCC	TCCGT TCCGC	GGGCG CGGGT	CGGCC TTCCG
1390	1400	1410	1420	1430	1440
TCTGT TCTAG	GGCCT GCTCC	TGCCG GGCAG	CTGCT TTAGA	AGGTC TCGAG	CTCCC TGTAC
1450	1460	1470	1480	1490	1500
CTTCC CAGGG	ATGAA CCGGG	CTTTC CTTCT	GGAAG GCGAG	GGTTC GGGCC	ACAGT GAGCG
1510	1520	1530	1540	1550	1560
AGGGC CAGGG	CGGTG GGGCG	GGCCA GAGGG	AAACC GGATC	AGTTG AGAGA	GAATC AAGAG
1570	1580	1590	1600	1610	1620
TAGCG GATGA	GCGCG TTCTG	GGGGC CGGCC	CGGAA GGCCCT	CGGGC GCGGG	CTGGG AGAAG
1630	1640	1650	1660	1670	1680
GAGTG GCGGG	AGGGC CGGCA	GGAGG CTCCC	GGGGC CTGGT	CGGGC CGGCT	GGGCC CCGAG
1690	1700	1710	1720	1730	1740
CGCAG TGGAA	GAAAG GGAGG	GCGGG TGCCC	GGTTG GGCCT	CGTGG CGAGC	TCACC TTGCC
1750	1760	1770	1780	1790	1800
CTGGC GGCTC	CGCCC GCGCG	CGACT TGGGA	GGAGC AGGGC	AGGGC CGCGG	GGCTT TGCAAT

Figure 4 (cont'd)

1810 1820 1830 1840 1850 1860
 TCTGG GACCG CCCCC TTCCA TTCCC GGGCC AGCGG CGAGC GGCAG CGAGG GGTGG AGCGC
 1870 1880 1890 1900 1910 1920
 CAGCT ACAGC ATGAG AGCGG GTGCC GCTCC TCCAC GCCTG CGGAC GCGTG GCGAG CGGAG
 1930 1940 1950 1960 1970
 GCAGC GCTGC CTGTT CGCGC C ATG GGG GCA CCG TGG GGC TCG CCG ACC GCG GCG
 Met Gly Ala Pro Trp Gly Ser Pro Thr Ala Ala
 1980 1990 2000 2010 2020
 GCG GCG GGG GCG GCG GCG TGG CCG CGA GCG GCG GCG CTG CCA TGG ACC GTC TGT
 Ala Gly Gly Arg Arg Gly Trp Arg Arg Gly Arg Gly Leu Pro Thr Val Cys
 2030 2040 2050 2060 2070 2080
 GTG CTG CCG CCG CCG CCG TTG ACG TGT ACG GCG CTG ATC ACC TAC GCT TCG TGG
 Val Leu Ala Ala Ala Gly Leu Thr Cys Thr Ala Leu Ile Thr Tyr Ala Cys Trp
 2090 2100 2110 2120 2130
 GGG CAG CTG CCG CCG CTG CCG TGG GCG TCG CCA ACC CCG TCG CGA CCG GTG GGC
 Gly Gln Leu Pro Pro Leu Pro Trp Ala Ser Pro Thr Pro Ser Arg Pro Val Gly
 2140 2150 2160 2170 2180 2190
 GTG CTG CTG TGG TGG GAG CCC TTC GGG GGG CCG GAT AGC GCC CCG AGG CCG CCC
 Val Leu Leu Trp Trp Glu Pro Phe Gly Gly Arg Asp Ser Ala Pro Arg Pro Pro
 2200 2210 2220 2230 2240
 CCT GAC TCG CCG CCG CCG TTC AAC ATC AGC GGC TGC CCG CTG CTC ACC GAC GCG
 Pro Asp Cys Pro Leu Arg Phe Asn Ile Ser Gly Cys Arg Leu Leu Thr Asp Arg
 2250 2260 2270 2280 2290
 GCG TCG TAC GGA GAG GCT CAG GCC GTG CTT TTC CAC CAC CCG GAC CTC GTG AAG
 Ala Ser Tyr Gly Glu Ala Gln Ala Val Leu Phe His His Arg Asp Leu Val Lys
 2300 2310 2320 2330 2340 2350
 GGG CCC CCG GAC TGG CCC CCG CCC TGG GGC ATC CAG GCG CAC ACT GCC GAG GAG
 Gly Pro Pro Asp Trp Pro Pro Pro Trp Gly Ile Gln Ala His Thr Ala Glu Glu
 2360 2370 2380 2390 2400
 GTG GAT CTG CCG GTG TTG GAC TAC GAG GAG GCA GCG GCG GCG GCA GAA GCC CTG
 Val Asp Leu Arg Val Leu Asp Tyr Glu Glu Ala Ala Ala Ala Glu Ala Leu
 2410 2420 2430 2440 2450 2460
 GCG ACC TCG AGC CCG AGG CCC CCG GCG CAG GCG TGG GTT TGG ATG AAC TTC GAG
 Ala Thr Ser Ser Pro Arg Pro Pro Gly Gln Arg Trp Val Trp Met Asn Phe Glu
 2470 2480 2490 2500 2510
 TCG CCC TCG CAC TCG CCG GGG CTG CGA AGC CTG GCA AGT AAC CTC TTC AAC TGG
 Ser Pro Ser His Ser Pro Gly Leu Arg Ser Leu Ala Ser Asn Leu Phe Asn Trp

Figure 4 (cont'd)

2520	2530	2540	2550	2560	
ACG CTC TCC TAC CGG GCG GAC TCG GAC GTC TTT GTG CCT TAT GGC TAC CTC TAC					
Thr Leu Ser Tyr Arg Ala Asp Ser Asp Val Phe Val Pro Tyr Gly Tyr Leu Tyr					
2570	2580	2590	2600	2610	2620
CCC AGA AGC CAC CCC GCG GAC CCG CCC TCA GGC CTG GCG CCG CCA CTG TCC AGG					
Pro Arg Ser Ser His Pro Gly Asp Pro Pro Ser Gly Leu Ala Pro Pro Leu Ser Arg					
2630	2640	2650	2660	2670	
AAA CAG GCG CTG GTG GCA TGG GTG GTG AGC CAC TGG GAC GAG CGC CAG GCC CGG					
Lys Gln Gly Leu Val Ala Trp Val Val Ser His Trp Asp Glu Arg Gln Ala Arg					
2680	2690	2700	2710	2720	2730
GTG CGC TAC TAC CAC CAA CTG AGC CAA CAT GTG ACC GTG GAC GTG TTC GGC CGG					
Val Arg Tyr Tyr His Gln Leu Ser Gln His Val Thr Val Asp Val Phe Gly Arg					
2740	2750	2760	2770	2780	
GGC GCG CCG GCG CAG CCG GTG CCC GAA ATT GCG CTC CTG CAC ACA GTG GCC CGC					
Gly Gly Pro Gly Gln Pro Val Pro Glu Ile Gly Leu Leu His Thr Val Ala Arg					
2790	2800	2810	2820	2830	
TAC AAG TTC TAC CTG GGT TTC GAG AAC TCG CAG CAC CTG GAT TAT ATC ACC GAG					
Tyr Lys Phe Tyr Leu Ala Phe Glu Asn Ser Gln His Leu Asp Tyr Ile Thr Glu					
2840	2850	2860	2870	2880	2890
AAG CTC TGG CCG AAC GCG TTG CTC GGT GGG GCG GTG CCG GTG GTG CTG GCC CCA					
Lys Leu Trp Arg Asn Ala Leu Leu Ala Gly Ala Val Pro Val Val Leu Gly Pro					
2900	2910	2920	2930	2940	
GAC CGT GCG AAC TAC GAG CGC TTT GTG CCC GCG GCG GCG TTC ATC CAC GTG GAC					
Asp Arg Ala Asn Tyr Glu Arg Phe Val Pro Arg Gly Ala Phe Ile His Val Asp					
2950	2960	2970	2980	2990	3000
GAC TTC CCA AGT GCG TCC TCC CTG GCC TCG TAC CTG GTT TTC CTC GAC CGC AAC					
Asp Phe Pro Ser Ala Ser Ser Leu Ala Ser Tyr Leu Leu Phe Leu Asp Arg Asn					
3010	3020	3030	3040	3050	
CCG GCG GTC TAT CCG CCG TAC TTC CAC TGG CCG CCG AGC TAC GCT GTC CAC ATC					
Pro Ala Val Tyr Arg Arg Tyr Phe His Trp Arg Arg Ser Tyr Ala Val His Ile					
3060	3070	3080	3090	3100	
AGC TCC TTC TGG GAC GAG CCT TGG TGC CCG GTG TGC CAG GCT GTA CAG AGG GCT					
Thr Ser Phe Trp Asp Glu Pro Trp Cys Arg Val Cys Gln Ala Val Gln Arg Ala					
3110	3120	3130	3140	3150	3160
GGG GAC CCG CCC AAG AGC ATA CCG AAC TTG GCG AGC TCG TTC GAG CCG TGA A					
Gly Asn Arg Pro Lys Ser Ile Arg Asn Leu Ala Ser Trp Phe Glu Arg ***					

Figure 4 (cont'd)

3170	3180	3190	3200	3210	3220
GCGGC GGTCC CCGGG AAGCG ACCCA GGGGA GGCCA AGTTG TCAGC TTTT GATCC TGTAC					
3230	3240	3250	3260	3270	3280
TGTGC ATCTC GTTGA CTGCC GCATC ATGGG AGTAA GTTCT TCAAA CAGCC ATTTT TGCTC					
3290	3300	3310	3320	3330	3340
TATGG GAAAA AAACG ATTTA CCAAT TAATA TTACT CAGCA CAGAG ATGGG GGCCC GGTTC					
3350	3360	3370	3380	3390	3400
CCATA TTTT TGCAC AGCTA GCAAT TGGG TCCCT TTGCT GCTGA TGGGC ATCAT TGTTC					
3410	3420	3430	3440	3450	3460
AGGGG TGAAG CAGGG CTTTC TTCTT CAGCT TGTAA CCAAT GCAGA AATGA AATAG CTTAG					
3470	3480	3490	3500	3510	3520
CGGCA AGAAG CCGTT GAGGC GGTTT CCTGA ATTTC CCCAT CTGCC ACAGG CCATA TTGTG					
3530	3540	3550	3560	3570	3580
GGCCC GTGCA GTTTC CAAAT CTCAT ACACA ACTGT TCCCG ATTCA CGTTT TTCTG GACCA					
3590	3600	3610	3620	3630	3640
AGGTG AAGCA AATTG GTGGT TGTAG AAGGA GCCTT GTTGG TGGAG AGTGG AAGGA CTGTG					
GCTGC AG					

Figure 7 (page 2)

$\alpha(1), 3\text{FT AA}$	Q A D A A V I V H H R E V M Y N P S A Q L
$\alpha(1), 3\text{FT DNA}$ (301)	CAGCAGACCGGCTCATCGTGCACACCGAGGTCATGTACAACCCAGTCGCCACGCTC
Levels FT DNA	CAGCAGACCGGTCATCGTGCACCACTGGGATATCATGTCCAAACCTTAAGTCACGCGCTC
$\alpha(1), 3\text{FT AA}$	P R S P R R Q G Q R W I W F S M E S P S
$\alpha(1), 3\text{FT DNA}$ (361)	CCACGCTCCCGAGGCGGAGGCGAGCGATGTGGTTTCAGCATGTGAGTCCCCGAAGC
Levels FT DNA	CCACCTTCCCGAGGCGGAGGCGAGCGCTGGATCTGGTTCAACTTTGGAGCCACACCCCTC
$\alpha(1), 3\text{FT AA}$	H C W Q L K A M D G Y F N L T M S Y R S
$\alpha(1), 3\text{FT DNA}$ (421)	CACCTGTGGCAGCTGAAGGCCATGAGCGATCTCAATCTCACCATGTCTCATCCGCGAC
Levels FT DNA	AACTGGCAGCACCTTGGAGGCCCTTGGACAGATACTTTCAATCTCACCATGTCTCATCCGCGAC
$\alpha(1), 3\text{FT AA}$	D S D I F T P Y G W L E P W S G Q P A H
$\alpha(1), 3\text{FT DNA}$ (481)	GACTCGGACATCTTCACGCCCTACGGCTGGGTGGAGCGTGGTCCGGCCAGCTGCCAC
Levels FT DNA	GACTCGGACATCTTCACGCCCTACGGCTGGGTGGAGCGGTGGTCCGGCCAGCTGCCAC
$\alpha(1), 3\text{FT AA}$	P P L N L S A K T E L V A W A V S N W G
$\alpha(1), 3\text{FT DNA}$ (541)	CCACCGCTCAACCTCTCGGCCAAGACCGAGTGGTGGCGCTGGGAGTGTCTCAACTGGGG
Levels FT DNA	CCACCGCTCAACCTCTCGGCCAAGACCGAGTGGTGGCGCTGGGCGGTGTCTCAACTGGGAAG
$\alpha(1), 3\text{FT AA}$	P N S A R V R Y Y Q S S L Q A H L K V D V
$\alpha(1), 3\text{FT DNA}$ (601)	CCAACTCCCGCAGGCTGGCTACTACCAAGAGCCGTGACGGCCCATCTCAAGTGGACGTG
Levels FT DNA	CCGAGCTCAGCAGGCTGGGCTACTACAGAGCCGTGACGGCTCATCTCAAGTGGACGTG

Figure 7 (page 3)

$\alpha(1.3)$ FT AA	Y G R S H K P L P Q G T M M E T L S R Y
$\alpha(1.3)$ FT DNA (661)	TACGGACGCTCCACAAAGCCCTGCCAGGAGAACCATGATGGAGACGCTGTCCCGGTAC
Lewis FT DNA	
	TACGG/CGCTCCACAAAGCCCTGCCAAGGGAGACCATGATGGAGACGCTGTCCCGGTAC
$\alpha(1.3)$ FT AA	K F Y L A F E N S L H P D Y I T E K L W
$\alpha(1.3)$ FT DNA (721)	AAGTTCTATCTGGGCTTCGAGAACTCCTTCACCCGAGCTACATCACCGAAGCTGTGG
Lewis FT DNA	
	AAGTTCTACCTGGGCTTCGAGAACTCCTTCACCCGAGCTACATCACCGAAGCTGTGG
$\alpha(1.3)$ FT AA	R N A L E A W A V P V L G P S R S N Y
$\alpha(1.3)$ FT DNA (781)	AGGAACGCCCTGGAGGCTGGCGCGTGGCTGGTCTGGGCCCCAGCAGAGAAGCACTAC
Lewis FT DNA	
	AGGAACGCCCTGGAGGCTGGCGCGTGGCTGGTCTGGGCCCCAGCAGAGAAGCACTAC
$\alpha(1.3)$ FT AA	E R F L P P D A F I H V D D F Q S P K D
$\alpha(1.3)$ FT DNA (841)	GAGAGGTTCTGCCACCCGAGCGCTTCATCCAGGTGGAGAGCTTCACAGAGCCCAAGGAC
Lewis FT DNA	
	GAGAGGTTCTGCCACCCGAGCGCTTCATCCAGGTGGAGAGCTTCACAGAGCCCAAGGAC
$\alpha(1.3)$ FT AA	L A R Y L Q E L D K D H A R Y L S Y F R
$\alpha(1.3)$ FT DNA (901)	CTGCCCGGTACCTGCAGAGCTGGACAAAGGACACCGCCGCTACCTGAGTACTTTTCGC
Lewis FT DNA	
	CTGCCCGGTACCTGCAGAGCTGGACAAAGGACACCGCCGCTACCTGAGTACTTTTCGC
$\alpha(1.3)$ FT AA	W R E T L R P R S F S W A L A F C K A C
$\alpha(1.3)$ FT DNA (961)	TGGCGGAGACGCTGGCGGCTCGCTCCTTCAGCTGGGCACTCGCTTTCTGCAAGGCTGC
Lewis FT DNA	
	TGGCGGAGACGCTGGCGGCTCGCTCCTTCAGCTGGGCACTGGATTTCTGCAAGGCTGC
$\alpha(1.3)$ FT AA	W K L Q E E S R Y Q T R G I A A W F T Stop
$\alpha(1.3)$ FT DNA (1021)	TGGAACTGCAGAGGAATCCAGGTACAGACACCGGC...ATAGGGCTTGGTTACCTGA
Lewis FT DNA	
	TGGAACTGCAGAGGAATCCAGGTACAGAGCGGTGGCGCATAGCGGCTTGGTTACCTGA

Figure 7 (page 4)

GAGGCTGGTGTGGGGCTGGGCTGCCAGGAACCTCAITTTCTGGGGCTCACCTGAGTG
GGGGCTCATCTACCTAAGGACTCGTTTGCCTGAAGCTTCACCTGCCTGAGGACTCACCT
GCCTGGGACGGTCACCTGTTGCAGCTTCACCTGCCTGGGGATTACCTACCTGGTCCCTC
ACTTTCCTGGGGCTCACCTGCTGGAGTCTTCGGTGGCCAGGTATGTCCCTTACCTGGGA
TTTCACATGCTGGCTTCCAGGAGCGTCCCTCGGAGCTGGCTGCTGGGATGTCTC
CTGGGACTTTGGCTTACTGGGACCTCGGCTGTTGGGACTTTACCTGCTGGGACCTGCT
CCAGAGACCTTCCACACTGAATCTCACCTGCTAGGACCTCACCTGCTGGGGACCTCAC
CCTGGAGGCACCTGGGGCCCTGGGAACT

Figure 8.

